

SEQUENCE LISTING

<110> Sanofi Pasteur

<120> Modified KSA and Uses Thereof

<130> API-03-17-PCT-US

<140> 10/584,378

<141> 2006-06-22

<150> PCT/US04/42980

<151> 2004-12-23

<150> 60/532,205

<151> 2003-12-23

<160> 22

<170> PatentIn version 3.3

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<223> Sense strand of ALVAC donor plasmid containing CEA-CAP1-6D-1,2 and p53 sequences shown in Fig. 1

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<212> DNA

<213> Artificial Sequence

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<223> Anti-sense strand of ALVAC donor plasmid containing CEA-CAP1-6D-1,2 and p53 sequences shown in Fig. 1

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tttttatttg tttatcccca aggcgcgtgt aaaggggctt ttcacggtgg actgcagatt	8160
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<210> 4
 <211> 2100
 <212> DNA
 <213> Artificial

<220>
 <223> mCEA(6D) sequence shown in Fig. 2A

<400> 4	
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acgccgttca atgtcgcaga ggggaaggag gtgcttctac ttgtccacaa tctgccccag	180
catctttttg gctacagctg gtacaaaggt gaaagagtgg atggcaaccg tcaaattata	240
ggatatgtaa taggaactca acaagctacc ccagggcccg catacagtgg tcgagagata	300
atatacccca atgcatccct gctgatccag aacatcatcc agaatgacac aggattctac	360
accctacacg tcataaagtc agatcttgtg aatgaagaag caactggcca gttccgggta	420
taccgggaac tccctaagcc ttctattagc tccaataata gtaagcctgt cgaagacaaa	480

gatgccgtcg cttttacatg cgagcccgaa actcaagacg caacatatct ctggtgggtg	540
aacaaccagt ccttgccctgt gtcccctaga ctccaactca gcaacggaaa tagaactctg	600
accctgttta acgtgaccag gaacgacaca gcaagctaca aatgcgaaac ccaaaatcca	660
gtcagcgcca ggaggtctga ttcagtgatt ctcaacgtgc tttacggacc cgatgctcct	720
acaatcagcc ctctaaacac aagctataga tcaggggaaa atctgaatct gagctgtcat	780
gccgctagca atcctcccgc ccaatacagc tggtttgtca atggcacttt ccaacagtcc	840
acccaggaac tgttcattcc caatattacc gtgaacaata gtggatccta cacgtgccaa	900
gctcacaata gcgacaccgg actcaaccgc acaaccgtga cgacgattac cgtgtatgag	960
ccacaaaaac cattcataac tagtaacaat tctaaccag ttgaggatga ggacgcagtt	1020
gcattaactt gtgagccaga gattcaaaat accacttatt tatggtgggt caataaccaa	1080
agtttgccgg ttagccacg cttgcagttg tctaatagata accgcacatt gacactcctg	1140
tccgttactc gcaatgatgt aggaccttat gagtgtggca ttcagaatga attatccgtt	1200
gatcactccg accctgttat ccttaatgtt ttgtatggcc cagacgaccc aactatatct	1260
ccatcataca cctactaccg tcccggcgtg aacttgagcc tttcttgcca tgcagcatcc	1320
aacccccctg cacagtactc ctggctgatt gatggaaaca ttcagcagca tactcaagag	1380
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aagccctcca tctccagcaa caactccaaa cccgtggagg acaaggatgc tgtggccttc	1560
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acaagaaatg acgcaagagc ctatgtatgt ggaatccaga actcagtgag tgcaaaccgc	1740
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gactcgtctt acctttcggg agcggacctc aacctctcct gccactcggc ctctaacca	1860
tccccgcagt attcttggcg tatcaatggg ataccgcagc aacacacaca agttctcttt	1920
atcgccaaaa tcacgcaaaa taataacggg acctatgcct gttttgtctc taacttggct	1980
actggccgca ataattccat agtcaagagc atcacagtct ctgcatctgg aacttctcct	2040
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<210> 5

<211> 2100

<212> DNA
<213> Artificial

<220>

<223> mCEA(6D, 1st & 2nd) sequence shown in Fig. 2A

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acgccgttca atgtcgcaga ggggaaggag gtgctttctac ttgtccacaa tctgccccag	180
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ggatatgtaa taggaactca acaagctacc ccagggtccc catacagtgg tcgagagata	300
atatacccca atgcatccct gctgatccag aacatcatcc agaatgacac aggattctac	360
accctacacg tcataaagtc agatcttgtg aatgaagaag caactggcca gttccgggta	420
taccgggagc tgccaagcc ctccatctcc agcaacaact ccaaaccgtg ggaggacaag	480
gatgctgtgg ccttcacctg tgaacctgag actcaggacg caacctacct gtggtgggta	540
aacaatcaga gcctcccggt cagtcccagg ctgcagctgt ccaatggcaa caggaccctc	600
actctattca atgtcacaag aaatgacaca gcaagctaca aatgtgaaac ccagaaccca	660
gtgagtgtca gggtcagtg ttcagtcac ctgaatgtcc tctatggccc ggatgcccc	720
accatttccc ctctaaacac atcttacaga tcaggggaaa atctgaacct ctctgccac	780
gcagcctcta acccacctgc acagtaactt tggtttgtca atgggacttt ccagcaatcc	840
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gccataact cagacactgg cctcaatagg accacagtca cgacgatcac agtctatgag	960
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gaccacagcg acccagtcac cctgaatgtc ctctatggcc cagacgacc caccatttcc	1260
ccctcatata cctattaccg tccaggggtg aacctcagcc tctcctgcca tgcagcctct	1320
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ctctttatct ccaacatcac tgagaagaac agcggactct atacctgcca ggccaataac	1440
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aagccctcca tctccagcaa caactccaaa cccgtggagg acaaggatgc tgtggccttc 1560
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<210> 6
<211> 9
<212> PRT
<213> Homo sapiens

<400> 6

Leu Leu Thr Phe Trp Asn Pro Pro Thr
1 5

<210> 7
<211> 10
<212> PRT
<213> Homo sapiens

<400> 7

Val Leu Tyr Gly Pro Asp Ala Pro Thr Ile
1 5 10

<210> 8
<211> 9
<212> PRT
<213> Homo sapiens

<400> 8

Ile Met Ile Gly Val Leu Val Gly Val
1 5

<210> 9
<211> 9
<212> PRT

<213> Homo sapiens

<400> 9

Gln Ile Ile Gly Tyr Val Ile Gly Thr
1 5

<210> 10

<211> 9

<212> PRT

<213> Homo sapiens

<400> 10

Lys Thr Cys Pro Val Gln Leu Trp Val
1 5

<210> 11

<211> 9

<212> PRT

<213> Homo sapiens

<400> 11

Ser Thr Pro Pro Pro Gly Thr Arg Val
1 5

<210> 12

<211> 11

<212> PRT

<213> Homo sapiens

<400> 12

Lys Thr Tyr Gln Gly Ser Tyr Gly Phe Arg Leu
1 5 10

<210> 13

<211> 10

<212> PRT

<213> Homo sapiens

<400> 13

Val Val Val Pro Tyr Glu Pro Pro Glu Val
1 5 10

<210> 14

<211> 314

<212> PRT

<213> Homo sapiens

<400> 14

Met Ala Pro Pro Gln Val Leu Ala Phe Gly Leu Leu Leu Ala Ala Ala
1 5 10 15

Thr Ala Thr Phe Ala Ala Ala Gln Glu Glu Cys Val Cys Glu Asn Tyr
20 25 30

Lys Leu Ala Val Asn Cys Phe Val Asn Asn Asn Arg Gln Cys Gln Cys
35 40 45

Thr Ser Val Gly Ala Gln Asn Thr Val Ile Cys Ser Lys Leu Ala Ala
50 55 60

Lys Cys Leu Val Met Lys Ala Glu Met Asn Gly Ser Lys Leu Gly Arg
65 70 75 80

Arg Ala Lys Pro Glu Gly Ala Leu Gln Asn Asn Asp Gly Leu Tyr Asp
85 90 95

Pro Asp Cys Asp Glu Ser Gly Leu Phe Lys Ala Lys Gln Cys Asn Gly
100 105 110

Thr Ser Thr Cys Trp Cys Val Asn Thr Ala Gly Val Arg Arg Thr Asp
115 120 125

Lys Asp Thr Glu Ile Thr Cys Ser Glu Arg Val Arg Thr Tyr Trp Ile
130 135 140

Ile Ile Glu Leu Lys His Lys Ala Arg Glu Lys Pro Tyr Asp Ser Lys
145 150 155 160

Ser Leu Arg Thr Ala Leu Gln Lys Glu Ile Thr Thr Arg Tyr Gln Leu
165 170 175

Asp Pro Lys Phe Ile Thr Ser Ile Leu Tyr Glu Asn Asn Val Ile Thr
180 185 190

Ile Asp Leu Val Gln Asn Ser Ser Gln Lys Thr Gln Asn Asp Val Asp
195 200 205

Ile Ala Asp Val Ala Tyr Tyr Phe Glu Lys Asp Val Lys Gly Glu Ser
210 215 220

Leu Phe His Ser Lys Lys Met Asp Leu Thr Val Asn Gly Glu Gln Leu
225 230 235 240

Asp Leu Asp Pro Gly Gln Thr Leu Ile Tyr Tyr Val Asp Glu Lys Ala
245 250 255

Pro Glu Phe Ser Met Gln Gly Leu Lys Ala Gly Val Ile Ala Val Ile
260 265 270

Val Val Val Val Ile Ala Val Val Ala Gly Ile Val Val Leu Val Ile
275 280 285

Ser Arg Lys Lys Arg Met Ala Lys Tyr Glu Lys Ala Glu Ile Lys Glu
290 295 300

Met Gly Glu Met His Arg Glu Leu Asn Ala
305 310

<210> 15
<211> 314
<212> PRT
<213> Artificial

<220>
<223> Modified KSA amino acid sequence as shown in Fig. 3

<400> 15

Met Ala Pro Pro Gln Val Leu Ala Phe Gly Leu Leu Leu Ala Ala Ala
1 5 10 15

Thr Ala Thr Phe Ala Ala Ala Gln Glu Glu Cys Val Cys Glu Asn Tyr
20 25 30

Lys Leu Ala Val Asn Cys Phe Val Asn Asn Asn Arg Gln Cys Gln Cys
35 40 45

Thr Ser Val Gly Ala Gln Asn Thr Val Ile Cys Ser Lys Leu Ala Ala
50 55 60

Lys Cys Leu Val Met Lys Ala Glu Met Asn Gly Ser Lys Leu Gly Arg
65 70 75 80

Arg Ala Lys Pro Glu Gly Ala Leu Gln Asn Asn Asp Gly Leu Tyr Asp
85 90 95

Pro Asp Cys Asp Glu Ser Gly Leu Phe Lys Ala Lys Gln Cys Asn Gly
100 105 110

Thr Ser Thr Cys Trp Cys Val Asn Thr Ala Gly Val Arg Arg Thr Asp
115 120 125

Lys Asp Thr Glu Ile Thr Cys Ser Glu Arg Val Arg Thr Tyr Trp Ile
130 135 140

Ile Ile Glu Leu Lys His Lys Ala Arg Glu Lys Pro Tyr Asp Ser Lys
145 150 155 160

Ser Leu Arg Thr Ala Leu Gln Lys Glu Ile Thr Thr Arg Tyr Gln Leu
165 170 175

Asp Pro Lys Phe Ile Thr Ser Val Leu Tyr Glu Asn Asn Val Ile Thr
180 185 190

Ile Asp Leu Val Gln Asn Ser Ser Gln Lys Thr Gln Asn Asp Val Asp
195 200 205

Ile Ala Asp Val Ala Tyr Tyr Phe Glu Lys Asp Val Lys Gly Glu Ser
210 215 220

Leu Phe His Ser Lys Lys Met Asp Leu Thr Val Asn Gly Glu Gln Leu
225 230 235 240

Asp Leu Asp Pro Gly Gln Thr Leu Ile Tyr Tyr Val Asp Glu Lys Ala
245 250 255

Pro Glu Phe Ser Met Gln Gly Leu Lys Ala Gly Val Ile Ala Val Ile
260 265 270

Val Val Val Val Ile Ala Val Val Ala Gly Ile Val Val Leu Val Ile
275 280 285

Ser Arg Lys Lys Arg Met Ala Lys Tyr Glu Lys Ala Glu Ile Lys Glu
290 295 300

Met Gly Glu Met His Arg Glu Leu Asn Ala
305 310

<210> 16
<211> 10
<212> PRT
<213> Homo sapiens

<400> 16

Gln Leu Asp Pro Lys Phe Ile Thr Ser Ile
1 5 10

<210> 17
<211> 10
<212> PRT
<213> Artificial

<220>

<223> Amino acid sequence of KSA peptide modified at amino acid 10

<400> 17

Gln Leu Asp Pro Lys Phe Ile Thr Ser Val
1 5 10

<210> 18
<211> 36
<212> DNA
<213> Homo sapiens

<400> 18

caaaatttat cacgagtgtg ttgtatgaga ataatg

36

<210> 19
<211> 36
<212> DNA
<213> Artificial

<220>

<223> Nucleotide sequence of KSA peptide modified at amino acid 10

<400> 19

cattattctc atacaacaca ctctgtgataa attttg

36

<210> 20
<211> 945
<212> DNA
<213> Artificial

<220>

<223> Modified KSA nucleic acid sequence as shown in Fig. 3B

<400> 20

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60

gccgcagctc aggaagaatg tgtctgtgaa aactacaagc tggccgtaaa ctgctttgtg	120
aataataatc gtcaatgcc a gtgtacttca gttggtgcac aaaatactgt catttgctca	180
aagctggctg ccaaatgttt ggtgatgaag gcagaaatga atggctcaaa acttgggaga	240
agagcaaaac ctgaaggggc cctccagaac aatgatgggc tttatgatcc tgactgcgat	300
gagagcgggc tctttaaggc caagcagtgc aacggcacct ccacgtgctg gtgtgtgaac	360
actgctgggg tcagaagaac agacaaggac actgaaataa cctgctctga gcgagtgaga	420
acctactgga tcatcattga actaaaacac aaagcaagag aaaaacctta tgatagtaaa	480
agtttgcgga ctgcacttca gaaggagatc acaacgcgtt atcaactgga tccaaaattt	540
atcacgagtg tgttgtatga gaataatgtt atcactattg atctggttca aaattcttct	600
caaaaaactc agaatgatgt ggacatagct gatgtggctt attattttga aaaagatgtt	660
aaaggtgaat ccttgtttca ttctaagaaa atggacctga cagtaaatgg ggaacaactg	720
gatctggatc ctggtcaaac tttaatttat tatgttgatg aaaaagcacc tgaattctca	780
atgcagggtc taaaagctgg tgttattgct gttattgtgg ttgtggtgat agcagttgtt	840
gctggaattg ttgtgctggt tatttccaga aagaagagaa tggcaaagta tgagaaggct	900
gagataaagg agatgggtga gatgcatagg gaactcaatg cataa	945

<210> 21
 <211> 9515
 <212> DNA
 <213> Artificial

<220>

<223> Sense strand of plasmid pT225KSAV-1 shown in Fig. 5

<400> 21	
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gccgcagctc aggaagaatg tgtctgtgaa aactacaagc tggccgtaaa ctgctttgtg	120
aataataatc gtcaatgcc a gtgtacttca gttggtgcac aaaatactgt catttgctca	180
aagctggctg ccaaatgttt ggtgatgaag gcagaaatga atggctcaaa acttgggaga	240
agagcaaaac ctgaaggggc cctccagaac aatgatgggc tttatgatcc tgactgcgat	300
gagagcgggc tctttaaggc caagcagtgc aacggcacct ccacgtgctg gtgtgtgaac	360
actgctgggg tcagaagaac agacaaggac actgaaataa cctgctctga gcgagtgaga	420
acctactgga tcatcattga actaaaacac aaagcaagag aaaaacctta tgatagtaaa	480

agtttgcgga ctgcacttca gaaggagatc acaacgcgtt atcaactgga tccaaaattt	540
atcacgagtg tgttgatga gaataatggt atcactattg atctggttca aaattcttct	600
caaaaaactc agaatgatgt ggacatagct gatgtggctt attattttga aaaagatggt	660
aaaggtgaat ccttgtttca ttctaagaaa atggacctga cagtaaatgg ggaacaactg	720
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